



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/687,204A

Source:

TFWO

Date Processed by STIC:

1-21-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/687,204A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.

6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or Artificial Sequence.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of <220> Sequence(s) 10-11, 13, 16 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.



IFWO

RAW SEQUENCE LISTING

DATE: 01/21/2005

PATENT APPLICATION: US/10/687,204A

TIME: 17:42:06

Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\01212005\J687204A.raw

4 <110> APPLICANT: Boehringer Ingelheim International GmbH
 6 <120> TITLE OF INVENTION: Composition for the Treatment of
 7 Infection by Flaviviridae Viruses
 10 <130> FILE REFERENCE: 13/118
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/687,204A
 C--> 13 <141> CURRENT FILING DATE: 2003-10-16
 15 <150> PRIOR APPLICATION NUMBER: US 60/421,900
 16 <151> PRIOR FILING DATE: 2002-10-29
 18 <160> NUMBER OF SEQ ID NOS: 16
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 28
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Primer
 30 <400> SEQUENCE: 1
 31 ctccgatccg gcgcccacac cggcctac 28
 33 <210> SEQ ID NO: 2
 34 <211> LENGTH: 33
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Artificial Sequence
 38 <220> FEATURE:
 39 <223> OTHER INFORMATION: primer
 41 <400> SEQUENCE: 2
 42 ctctctagat cagcactctt ccatttcacg gaa 33
 44 <210> SEQ ID NO: 3
 45 <211> LENGTH: 36
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Artificial Sequence
 49 <220> FEATURE:
 50 <223> OTHER INFORMATION: primer
 52 <400> SEQUENCE: 3
 53 ctctctagat cagcactctt ccatttcacg gaactc 36
 55 <210> SEQ ID NO: 4
 56 <211> LENGTH: 34
 57 <212> TYPE: DNA
 58 <213> ORGANISM: Artificial Sequence
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: primer
 63 <400> SEQUENCE: 4
 64 ctccgatccg gcgcccacac cggcctactc ccaa 34
 66 <210> SEQ ID NO: 5

Does Not Comply
 Corrected Diskette Needed
 (pg. 2-3)

RAW SEQUENCE LISTING

DATE: 01/21/2005

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TIME: 17:42:06

Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\01212005\J687204A.raw

67 <211> LENGTH: 16
 68 <212> TYPE: PRT
 69 <213> ORGANISM: HCV peptide
 71 <400> SEQUENCE: 5
 72 Pro Asp Arg Glu Val Leu Tyr Arg Glu Phe Asp Glu Met Glu Glu Cys
 73 1 5 10 15
 76 <210> SEQ ID NO: 6
 77 <211> LENGTH: 28
 78 <212> TYPE: DNA
 79 <213> ORGANISM: Artificial Sequence
 81 <220> FEATURE:
 82 <223> OTHER INFORMATION: primer
 84 <400> SEQUENCE: 6
 85 ctccgatccg gctcccatta ctgcttac 28
 87 <210> SEQ ID NO: 7
 88 <211> LENGTH: 43
 89 <212> TYPE: DNA
 90 <213> ORGANISM: Artificial Sequence
 92 <220> FEATURE:
 93 <223> OTHER INFORMATION: primer
 95 <400> SEQUENCE: 7
 96 gacgcgtcga cgcggccgct cagcactctt ccatttcact gaa 43
 98 <210> SEQ ID NO: 8
 99 <211> LENGTH: 31
 100 <212> TYPE: DNA
 101 <213> ORGANISM: Artificial Sequence
 103 <220> FEATURE:
 104 <223> OTHER INFORMATION: primer
 106 <400> SEQUENCE: 8
 107 ctccgatccg gccccgatca cagcatcacgc c 31
 109 <210> SEQ ID NO: 9
 110 <211> LENGTH: 41
 111 <212> TYPE: DNA
 112 <213> ORGANISM: Artificial Sequence
 114 <220> FEATURE:
 115 <223> OTHER INFORMATION: primer
 117 <400> SEQUENCE: 9
 118 caccgctcga gtcagcattc ttccatctca tcatattgtt g
 120 <210> SEQ ID NO: 10
 121 <211> LENGTH: 11
 122 <212> TYPE: PRT
 123 <213> ORGANISM: Artificial Sequence
 125 <220> FEATURE:
 126 <223> OTHER INFORMATION: Asp at position 1 is linked to anthranilyl
 128 <223> OTHER INFORMATION: Xaa at position 6 is aminobutyric acid [C(O)-O]
 130 <223> OTHER INFORMATION: Xaa at position 9 is (3-nitro)tyrosine
 W--> 132 <400> 10
 W--> 133 Asp Asp Ile Val Pro Xaa Ala Met Xaa Thr Trp
 134 1 5 10

See item #10 on error summary Sheet.

pls explain source of genetic material.

(see item #11 on error summary Sheet.)

RAW SEQUENCE LISTING

DATE: 01/21/2005

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TIME: 17:42:06

Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\01212005\J687204A.raw

137 <210> SEQ ID NO: 11
 138 <211> LENGTH: 11
 139 <212> TYPE: PRT
 140 <213> ORGANISM: Artificial Sequence
 142 <220> FEATURE:
 143 <223> OTHER INFORMATION: Xaa at position 6 is aminobutyric acid
 145 <400> SEQUENCE: 11
 W--> 146 Asp Asp Ile Val Pro Xaa Ala Met Tyr Thr Trp
 147 1 5 10
 150 <210> SEQ ID NO: 12
 151 <211> LENGTH: 12
 152 <212> TYPE: PRT
 153 <213> ORGANISM: HCV Peptide
 155 <400> SEQUENCE: 12
 156 Asp Asp Ile Val Pro Cys Ser Met Ser Tyr Thr Trp
 157 1 5 10
 160 <210> SEQ ID NO: 13
 161 <211> LENGTH: 11
 162 <212> TYPE: PRT
 163 <213> ORGANISM: Artificial Sequence
 165 <220> FEATURE:
 166 <223> OTHER INFORMATION: Xaa is at position 1 is anthranilyl-Asp
 168 <223> OTHER INFORMATION: Xaa at position 2 is (d)Glu
 170 <223> OTHER INFORMATION: Xaa at position 6 is norvaline[C(O)-O]
 172 <223> OTHER INFORMATION: Xaa at position 9 is (3-nitro)tyrosine
 W--> 174 <400> 13
 W--> 175 Xaa Xaa Ile Val Pro Xaa Ala Met Xaa Thr Trp
 176 1 5 10
 179 <210> SEQ ID NO: 14
 180 <211> LENGTH: 30
 181 <212> TYPE: DNA
 182 <213> ORGANISM: Artificial Sequence
 184 <220> FEATURE:
 185 <223> OTHER INFORMATION: primer
 187 <400> SEQUENCE: 14
 188 cgcataatggc acctttttacg ctgcagtgtc
 190 <210> SEQ ID NO: 15
 191 <211> LENGTH: 33
 192 <212> TYPE: DNA
 193 <213> ORGANISM: Artificial Sequence
 195 <220> FEATURE:
 196 <223> OTHER INFORMATION: primer
 198 <400> SEQUENCE: 15
 199 cgcgcgctcg agacactcct ccacgatttc ttc
 201 <210> SEQ ID NO: 16
 202 <211> LENGTH: 9
 203 <212> TYPE: PRT
 204 <213> ORGANISM: Artificial Sequence
 206 <220> FEATURE:

Needs explanation
 See item #11 on error summary sheet.

See item #10 on error summary sheet.

Same error
 See item #11 on error summary sheet.

Same error

RAW SEQUENCE LISTING

DATE: 01/21/2005

PATENT APPLICATION: US/10/687,204A

TIME: 17:42:06

Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\01212005\J687204A.raw

207 <223> OTHER INFORMATION: Xaa at position 1 is acetylated-Asp

209 <223> OTHER INFORMATION: Xaa at position 3 is Asp (EDANS)

211 <223> OTHER INFORMATION: Xaa at position 6 is amino butyric acid [C(O)-O]

213 <223> OTHER INFORMATION: Xaa at position 9 is Lys[DABCYL]

W--> 215 <400> 16

W--> 216 Xaa Glu Xaa Glu Glu Xaa Ala Ser Xaa

217 1

5

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/687,204A

DATE: 01/21/2005
TIME: 17:42:07

Input Set : A:\13_118 Final Sequences.txt
Output Set: N:\CRF4\01212005\J687204A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 6,9
Seq#:11; Xaa Pos. 6
Seq#:13; Xaa Pos. 1,2,6,9
Seq#:16; Xaa Pos. 1,3,6,9

VARIABLE LOCATION SUMMARY

DATE: 01/21/2005

PATENT APPLICATION: US/10/687,204A

TIME: 17:42:07

Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\01212005\J687204A.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:10; Xaa Pos. 6,9

Seq#:11; Xaa Pos. 6

Seq#:13; Xaa Pos. 1,2,6,9

Seq#:16; Xaa Pos. 1,3,6,9

VERIFICATION SUMMARY

DATE: 01/21/2005

PATENT APPLICATION: US/10/687,204A

TIME: 17:42:07

Input Set : A:\13_118 Final Sequences.txt

Output Set: N:\CRF4\01212005\J687204A.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:132 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:133 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:10
L:133 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:10
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:146 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:11
L:146 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:11
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:174 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:175 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13
L:175 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:13
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:215 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:216 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:16
L:216 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:16
L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0